







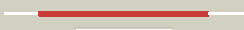















Phyre2

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Description	Q9BUP3
Date	Sat Jun 16 10:42:12 BST 2012
Unique Job ID	f3eda0738004930c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bkaa1	 Alignment		100.0	100	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
2	d2fmua1	 Alignment		100.0	92	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
3	c1z7eC_	 Alignment		100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
4	d2a35a1	 Alignment		99.9	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	c3oh8A_	 Alignment		99.9	16	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
6	c1z45A_	 Alignment		99.9	16	PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
7	c2qn9B_	 Alignment		99.9	16	PDB header: lyase Chain: B: PDB Molecule: udp-glcnac c6 dehydratase; PDBTitle: crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
8	d1i24a_	 Alignment		99.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
9	d1y1pa1	 Alignment		99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
10	c2zklA_	 Alignment		99.9	17	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
11	c2qx7A_	 Alignment		99.9	14	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum

12	c2iodD_	Alignment		99.9	18	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroflavonol 4-reductase; PDBTitle: binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
13	d1hdoa_	Alignment		99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	d2b69a1	Alignment		99.9	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
15	c2b69A_	Alignment		99.9	13	PDB header: lyase Chain: A: PDB Molecule: udp-glucuronate decarboxylase 1; PDBTitle: crystal structure of human udp-glucuronic acid decarboxylase
16	c3e8xA_	Alignment		99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad-dependent epimerase/dehydratase; PDBTitle: putative nad-dependent epimerase/dehydratase from bacillus halodurans.
17	c2hunB_	Alignment		99.9	12	PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase; PDBTitle: crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
18	c3nzoB_	Alignment		99.9	13	PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
19	c2p4hX_	Alignment		99.9	16	PDB header: plant protein Chain: X: PDB Molecule: vestitone reductase; PDBTitle: crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
20	c2x4gA_	Alignment		99.9	17	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
21	d1qyda_	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
22	d1oc2a_	Alignment	not modelled	99.9	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	d2q46a1	Alignment	not modelled	99.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
24	c3c1oA_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol synthase; PDBTitle: the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
25	c2v6gA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
26	c3dqpA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase ylbe; PDBTitle: crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
27	c3qvoA_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nmra family protein; PDBTitle: structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
28	c3vpsB_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of a novel nad dependent-ndp-hexosamine 5,6-dehydratase,2 tuna, involved in tunicamycin biosynthesis
						PDB header: oxidoreductase

29	c2rh8A_	Alignment	not modelled	99.8	18	Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera
30	c2hrzA_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: the crystal structure of the nucleoside-di-phosphate-sugar epimerase2 from agrobacterium tumefaciens
31	c3e48B_	Alignment	not modelled	99.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural_genomics3 consortium target zr319
32	d1qyca_	Alignment	not modelled	99.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c2gasA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: isoflavone reductase; PDBTitle: crystal structure of isoflavone reductase
34	c4egbC_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: C: PDB Molecule: ddtp-glucose 4,6-dehydratase; PDBTitle: 3.0 angstrom resolution crystal structure of dtdp-glucose 4,6-2 dehydratase (rfbb) from bacillus anthracis str. ames in complex with3 nad
35	c2q1wC_	Alignment	not modelled	99.8	13	PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
36	c2pzbB_	Alignment	not modelled	99.8	10	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme2 wbmh in complex with nad and udp
37	c3lu1C_	Alignment	not modelled	99.8	12	PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase
38	c3dhnA_	Alignment	not modelled	99.8	19	PDB header: isomerase, lyase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
39	d1xgka_	Alignment	not modelled	99.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
40	d1r6da_	Alignment	not modelled	99.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
41	c2exxB_	Alignment	not modelled	99.8	13	PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
42	d1db3a_	Alignment	not modelled	99.8	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
43	c3sxpD_	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: D: PDB Molecule: adp-l-glycero-d-mannoheptose-6-epimerase; PDBTitle: crystal structure of helicobacter pylori adp-l-glycero-d-manno-2 heptose-6-epimerase (rfad, hp0859)
44	c3i5mA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
45	d1e6ua_	Alignment	not modelled	99.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	c3rfxB_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: uronate dehydrogenase; PDBTitle: crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
47	c2yy7B_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
48	c2q1uA_	Alignment	not modelled	99.8	11	PDB header: sugar binding protein Chain: A: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+ and udp
49	c2vrcD_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
50	c3iusB_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss
51	c1n7gB_	Alignment	not modelled	99.8	12	PDB header: lyase Chain: B: PDB Molecule: gdp-d-mannose-4,6-dehydratase; PDBTitle: crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
52	c2z1mC_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
						Fold: NAD(P)-binding Rossmann-fold domains

53	d1rkxa_	Alignment	not modelled	99.8	16	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
54	c2vdyA_	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine adenosyltransferase 2 subunit beta; PDBTitle: crystal structure of human s-adenosylmethionine synthetase2 2, beta subunit in orthorhombic crystal form
55	c3ew7A_	Alignment	not modelled	99.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo0794 protein; PDBTitle: crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
56	c3enkB_	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
57	c3h2sA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh-flavin reductase; PDBTitle: crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
58	d1vl0a_	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	c3ay3C_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogenase from2 chromohalobacter salexigens
60	d1wvga1	Alignment	not modelled	99.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
61	c3m2pD_	Alignment	not modelled	99.8	11	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4-epimerase; PDBTitle: the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
62	d1sb8a_	Alignment	not modelled	99.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c3sc6F_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: F: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
64	d2c5aa1	Alignment	not modelled	99.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	d1n7ha_	Alignment	not modelled	99.8	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	d1eq2a_	Alignment	not modelled	99.8	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
67	d1bxka_	Alignment	not modelled	99.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	d1n2sa_	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
69	c2c20D_	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase
70	d1t2aa_	Alignment	not modelled	99.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
71	c3icpA_	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
72	c1t2aC_	Alignment	not modelled	99.8	13	PDB header: structural genomics,lyase Chain: C: PDB Molecule: gdp-mannose 4,6 dehydratase; PDBTitle: crystal structure of human gdp-d-mannose 4,6-dehydratase
73	d1kewa_	Alignment	not modelled	99.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
74	d1ek6a_	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c3eheB_	Alignment	not modelled	99.8	12	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase (gale-1); PDBTitle: crystal structure of udp-glucose 4 epimerase (gale-1) from2 archaeoglobus fulgidus
76	c3a1nB_	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: ndp-sugar epimerase; PDBTitle: crystal structure of l-threonine dehydrogenase from hyperthermophilic2 archaeon thermoplasma volcanium
77	d1z45a2	Alignment	not modelled	99.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	c2pk3B_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase

79	c2ggsB	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 273aa long hypothetical dtdp-4-dehydrorhamnose PDBTitle: crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
80	d1orra	Alignment	not modelled	99.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
81	d1rpna	Alignment	not modelled	99.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	c3gpiA	Alignment	not modelled	99.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
83	c2zcuA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized oxidoreductase ytfg; PDBTitle: crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
84	d1gy8a	Alignment	not modelled	99.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	c2p5uC	Alignment	not modelled	99.7	17	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
86	c3r6dA	Alignment	not modelled	99.7	16	PDB header: lyase, isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of nad-dependent epimerase/dehydratase from2 veillonella parvula dsm 2008 with cz-methylated lysine
87	c3slgB	Alignment	not modelled	99.7	16	PDB header: transferase Chain: B: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
88	c2x86K	Alignment	not modelled	99.7	12	PDB header: isomerase Chain: K: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: agme bound to adp-b-mannose
89	d2bla1	Alignment	not modelled	99.7	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	d1udca	Alignment	not modelled	99.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
91	c2jahB	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
92	c3un1D	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
93	c2dteB	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase related protein; PDBTitle: structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt)2 in complex with nadh
94	c3f9iB	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 rickettsia prowazekii
95	c3p19A	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
96	d1ulsa	Alignment	not modelled	99.3	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	c3ai3A	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-sorbose reductase; PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
98	d1jtva	Alignment	not modelled	99.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
99	c3cxtA	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
100	c3lylB	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acyl carrier protein reductase, fabg2 from francisella tularensis
101	d1sbya1	Alignment	not modelled	99.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
102	c3ijrf	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
						Fold: NAD(P)-binding Rossmann-fold domains

103	d1fmca_	Alignment	not modelled	99.3	18	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
104	d2gdza1	Alignment	not modelled	99.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	d1bdba_	Alignment	not modelled	99.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
106	c2p68A_	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
107	c3grkE_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nah); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
108	c3pgxB_	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of a putative carveol dehydrogenase from2 mycobacterium paratuberculosis bound to nicotinamide adenine3 dinucleotide
109	d1uzma1	Alignment	not modelled	99.2	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
110	d1iy8a_	Alignment	not modelled	99.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
111	c3toxG_	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
112	c4dqxB_	Alignment	not modelled	99.2	10	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
113	c3ak4C_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
114	c4dmmA_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: 3-oxoacyl-[acyl-carrier-protein] reductase from synechococcus2 elongatus pcc 7942 in complex with nadp
115	c3rkuC_	Alignment	not modelled	99.2	22	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase ymr226c; PDBTitle: substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
116	c3ioyB_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793)2 from novosphingobium aromaticivorans
117	d1xkqa_	Alignment	not modelled	99.2	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	d1o0ea_	Alignment	not modelled	99.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
119	d1mlda1	Alignment	not modelled	99.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
120	d2ag5a1	Alignment	not modelled	99.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases